RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/677, 956 B

Source: _____ IFW16

Date Processed by STIC: _____ 09/14/2006

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RAW SEQUENCE LISTING   DATE: 09/14/2006
PATENT APPLICATION: US/10/677,956B   TIME: 15:32:14

Input Set : **E:\16988.ST25.txt**
Output Set: **N:\CRF4\09142006\J677956B.raw**

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 5 <110> APPLICANT: Zebedee, Suzanne
 6         Inchauspe, Genevieve
 7         Nasoff, Marc S.
 8         Prince, Alfred M.
10 <120> TITLE OF INVENTION: METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT
VIRAL ANTIGENS
12 <130> FILE REFERENCE: 323-100USD
14 <140> CURRENT APPLICATION NUMBER: 10/677,956B
15 <141> CURRENT FILING DATE: 2003-10-01
17 <150> PRIOR APPLICATION NUMBER: 08/931,855
18 <151> PRIOR FILING DATE: 1997-09-16
20 <150> PRIOR APPLICATION NUMBER: 08/563,733
21 <151> PRIOR FILING DATE: 1995-11-08
23 <150> PRIOR APPLICATION NUMBER: 08/272,271
24 <151> PRIOR FILING DATE: 1994-07-08
26 <150> PRIOR APPLICATION NUMBER: 07/616,369
27 <151> PRIOR FILING DATE: 1990-11-21
29 <150> PRIOR APPLICATION NUMBER: 07/573,643
30 <151> PRIOR FILING DATE: 1990-08-27
32 <160> NUMBER OF SEQ ID NOS: 74
34 <170> SOFTWARE: PatentIn version 3.3
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 795
38 <212> TYPE: DNA
39 <213> ORGANISM: Human immunodeficiency virus
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43 <221> NAME/KEY: CDS
44 <222> LOCATION: (16)..(789)
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49                1           5                   10
51 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta    99
52 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
53         15                  20                  25
55 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta   147
56 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
57     30                  35                  40
59 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg   195
60 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
61 45                  50                  55                  60
63 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag   243
64 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
65                 65                  70                  75
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72 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
73             95                 100                 105
75 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct      387
76 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
77     110                 115                 120
79 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat      435
80 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
81 125                 130                 135                 140
83 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa      483
84 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
85                 145                 150                 155
87 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act      531
88 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
89             160                 165                 170
91 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa      579
92 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
93             175                 180                 185
95 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa      627
96 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
97     190                 195                 200
99 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag      675
100 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
101 205                 210                 215                 220
103 gga gta gga gga ccc aaa aat caa caa tta tta tcc tta tgg ggg tgt     723
104 Gly Val Gly Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys
105                 225                 230                 235
107 aaa ggg aaa ctt gtt tgt tat act tcc gtt aaa tgg aat gga ccc ggc     771
108 Lys Gly Lys Leu Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
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119 <213> ORGANISM: Human immunodeficiency virus
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128             20                  25                  30
131 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
132         35                  40                  45
135 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
136     50                  55                  60
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140 65                  70              75                  80
143 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
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148             100             105             110
151 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
152         115             120             125
155 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
156     130             135             140
159 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
160 145             150             155                 160
163 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
164             165             170             175
167 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
168     .       180             185             190
171 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
172         195             200             205
175 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
176     210             215             220
179 Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu
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183 Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro·Gly His Lys Ala Arg
184             245             250             255
187 Val Leu
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193 <212> TYPE: DNA
194 <213> ORGANISM: Human immunodeficiency virus
197 <220> FEATURE:
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199 <222> LOCATION: (16)..(789)
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206 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
207 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
208         15              20                  25
210 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta     147
211 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
212     30              35                  40
214 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg     195
215 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
216 45              50                  55                  60
218 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag     243
219 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
220             65              70                  75
222 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att     291
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223 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
224               80               85               90
226 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act      339
227 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
228           95               100               105
230 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct      387
231 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
232       110               115               120
234 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat      435
235 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
236 125               130               135               140
238 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa      483
239 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
240               145               150               155
242 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act      531
243 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
244               160               165               170
246 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa      579
247 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
248           175               180               185
250 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa      627
251 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
252       190               195               200
254 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag      675
255 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
256 205               210               215               220
258 gga gta gga gga ccc aaa aat caa caa aga tta aat tta tgg ggg tgt      723
259 Gly Val Gly Gly Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys
260               225               230               235
262 aaa ggg aaa ctt att tgt tat act tcc gtt aaa tgg aat gga ccc ggc      771
263 Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
264               240               245               250
266 cat aag gca aga gtt ttg taataa                                       795
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268           255
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273 <212> TYPE: PRT
274 <213> ORGANISM: Human immunodeficiency virus
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283           20               25               30
286 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
287       35               40               45
290 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
291 50               55               60
294 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
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295 65                    70                 75                 80
298 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
299                    85                 90                 95
302 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
303                    100                105                110
306 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
307                    115                120                125
310 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
311         130                135                140
314 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
315 145                150                155                160
318 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
319                    165                170                175
322 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
323                    180                185                190
326 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
327         195                200                205
330 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
331         210                215                220
334 Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu
335 225                230                235                240
338 Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg
339                    245                250                255
342 Val Leu
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347 <211> LENGTH: 795
348 <212> TYPE: DNA
349 <213> ORGANISM: Human immunodeficiency virus
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353 <221> NAME/KEY: CDS
354 <222> LOCATION: (16)..(789)
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359                    1                 5                10
361 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta        99
362 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
363         15                20                25
365 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta       147
366 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
367         30                35                40
369 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg       195
370 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
371 45                50                55                60
373 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag       243
374 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
375                    65                70                75
377 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att       291
378 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/14/2006
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<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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VERIFICATION SUMMARY   DATE: 09/14/2006
PATENT APPLICATION: **US/10/677,956B**   TIME: 15:32:15

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